

EPA Comments Appendix E: Round 2 Comprehensive Site Characterization Summary and Data Gaps Report  
June 16, 2008

Introduction:

EPA has previously provided comments on various sections the Round 2 Comprehensive Site Characterization Summary and Data Gaps Report (Round 2 Report). These comments on Appendix E of the Round 2 Report represent EPA's final comments on the Round 2 Report.

Appendix E presented information on the development of biota-sediment accumulation factors (BSAFs) and the site specific food web model for the Portland Harbor Superfund Site. These evaluations are considered critical to the development of cleanup goals for bioaccumulative chemicals such as polychlorinated biphenyls (PCBs), organochlorine pesticides (e.g., 4,4'-DDT) and polychlorinated dibenzo-p-dioxins and furans (PCDD/PCDF). The model also generates information that can be used to estimate dioxin-like toxicity equivalency quotients (TEQ's) for PCB, dioxin and furan congeners that contribute to the toxic mechanism of action of 2,3,7,8-tetrachlorodibenzo-p-dioxin (2,3,7,8-TCDD), the most toxic of the dioxin congeners.

**General Comments:**

Overall Model Approach:

The overall modeling approach is sound and follows appropriate guidance documents. The utility of the FWM for developing clean-up goals and for predicting potential remediation impact is uncertain, as is always the case when a FWM calibrated to existing conditions is used to predict future concentrations of chemicals in sediment and tissues, either with or without site remediation. The main weaknesses of the current approach include: (i) the use of the complex Arnot and Gobas model with multiple generic parameters with large uncertainty and unknown site specificity and applicability to Portland Harbor; (ii) basing the primary model predictions on a model calibration using a very limited tissue data set that excludes the major biological sampling during Round 3 of the Portland Harbor RI process (although in fairness, the Round 3 data were not available at the time the Round 2 report was prepared); and (iii) limited incorporation of spatial factors affecting biotic exposure of some modeled species to and uptake of contaminants (e.g., species behavior, contaminant distribution, etc). Spatial factors and temporal variance will play a significant role in developing an understanding of current risks and evaluating the risk-reduction benefits of remedy options, at least for species such as bass and sculpin, where empirical evidence exists that tissue residues vary as a function of measured sediment PCB concentrations.

Model Parameterization:

The Arnot & Gobas (2004) model, an extension of the "original" Gobas model (1995), incorporates aspects of fish physiology and contaminant transport across gut membranes that have little to do with the management decision to be made with the FWM. The key with any

food web model and model application is that it should provide a tool with which site managers can base their upcoming management decisions. Increased model complexity such as is present in the Arnot and Gobas model relative to other modeling approaches always leads to more options in terms of calibration parameters, more unknowns, more data requirements, and increased uncertainty. Although there has been a longstanding agreement between EPA and the LWG to use the Arnot and Gobas food web model at Portland Harbor, it should be recognized that the Portland Harbor food web model may not offer the desired level of increased realism over simpler modeling approaches such as site specific BSAFs if that increased realism is based on literature values for the new parameters. Indeed, dietary absorption efficiency of lipids and porewater ventilation by benthic invertebrates are two key model parameters that are reasonably uncertain and for which there will never be site-specific measurements.

The Portland Harbor Food web model relied on a series of modifications to the Arnot and Gobas model. In particular, the model included the optimization of 21 internal parameters. It is unclear whether these modifications were appropriate in all cases. In general, EPA does not support modification of the internal parameters of the Arnot and Gobas model. Modification of these parameters suggest that the Portland Harbor data is of better quality than those used by Arnot and Gobas to build and validate their model; this may not be the case. Given the complexities of the site, it is unclear ~~has not been demonstrated that the optimized~~ whether the site specific data internal model parameters are in fact superior to the Arnot and Gobas defaults, nor is it clear they ~~and~~ should be used as the basis for parameterization of the model. Instead of fine tuning values to get agreement, it may be more appropriate to ~~to limit changes to the model to site specific information, leaving most of the internal model parameters unchanged~~ evaluate the uncalibrated model to test model performance.

There also appears to have been a change in the equation used to estimate water contaminant concentrations (Equation 6 of Attachment E1 in the Round 2 Report) compared to the version of the equation given in Morrison et al. (1997) (Equation 15 of the Morrison et al. 1997 paper). Since organic carbon analyses for Portland Harbor are from samples filtered through a large pore size filter (0.5µm), EPA recommends that the model return to the use of the Gobas equation that calculates the bioavailable fraction from a total contaminant measure.

#### Use of Surface Weighted Average Concentrations:

The LWG used surface weighted average concentrations (SWACs) to develop average sediment concentrations. This is the same issue we recently addressed in the review of the Duwamish River FWM also developed by Woodward, so we would like comment on the appropriateness of this approach.

The use of a site wide SWAC value assumes that the organism uses the entire site in the same proportions as the size of the various Thiessen polygons. This assumption somewhat conflicts with a standard FWM assumption of equal use of all areas being modeled, not the weighted use of the site as defined by Thiessen polygons. Although not necessarily wrong, it is not possible to determine the effects of the use of SWACs for sediment chemical concentrations on model

predictions without also using the more commonly used arithmetic mean sediment concentration. Further, the SWAC was computed assuming equal chemical bioavailability across the site, and this is not true based upon the data from the lab worm and clam testing data, and the clam field data. Because model is constructed using a single water and sediment input concentrations, some type of averaging will be required.

The Portland Harbor Foodweb model relied on the use of surface weighted average concentrations (SWACs) to develop average sediment concentrations. The use of a site-wide SWAC value assumes that the organism uses the entire site. Further, the SWAC was computed assuming equal chemical bioavailability across the site. Based on the laboratory worm and clam bioaccumulation studies, an assumption of equal chemical bioavailability may not be appropriate. Because model is constructed using a single water and sediment input concentrations, some type of averaging will be required. One possibility that should be considered is to drive the food web model with residues in the worm and clam data rather than the residues in the sediment in order to consider chemical bioavailability

#### Evaluation of Model Performance:

We currently are not convinced that the model predictions are sufficiently accurate for all chemicals and species for which predictions are required. For example, some of the PCB TEQ in tissue predictions (particularly PCB TEQs in birds, as shown in Figure 3-3 of the FWM) are no better than between 5x and 10x of the empirical data, which we do not believe allows site managers to have confidence in the FWM output for those parameters.

We suspect (but don't know) that issues with the TEQ predictions are influenced by data quality issues. Given how the model works for other non-polar organic chemicals, there is no reason why the model should not have similar predictive ability for the TEQ chemicals. One recommendation is to rerun the model using the specific PCB congeners that contribute to the total TEQ. The specific congeners have better defined log K<sub>OW</sub> values than does total PCB. The TEQ estimates from the individual congeners could then be summed outside of the FWM to see if the predictions are more accurate than the current values of SPAF for PCB TEQs in birds. EPA is not comfortable using the PCB TEQ in birds predictions from the FWM for any purpose at this time in the RI/FS.

Similarly, the model predictions for PCBs in crayfish (Table 3-26 of the FWM) are poor, with only 6 of 26 predicted tissue values having a SPAF less than 5.0. Although we have several thoughts on why this is, largely relating to the dietary estimates used, we have to admit we do not have an easily applied recommendation to improve the crayfish predictions. EPA is not comfortable using the crayfish predictions for any purpose at this time in the RI/FS.

Arnot and Gobas recommend evaluating the ratio of predicted and observed concentrations to test model performance. Currently, the Portland Harbor food web model does not use an estimate of observed vs. predicted values to provide an estimate of uncertainty because of its over calibration. The data may be used to determine how uncertain the model is. This is different than model uncertainty analysis, which should largely be avoided because many parameters are correlated. It is therefore difficult to apply Monte Carlo simulations of

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Commented [MM1]: Is this true? This is Jennifer's comment. However, it seems to me that the SPAF presented in the report evaluates model performance.

uncertainty. The only parameters that are NOT correlated and a true uncertainty analysis could be performed would be lipid content, temperature, and  $K_{ow}$ .

Model predictions for TEQ PCBs are no better than between 5x and 10x of the empirical data. Because the model appears to work well for other non-polar organic chemicals, investigation into the cause of this poor performance is recommended. For example, a review of the TEQ data to ensure that data quality issues are not resulting in poor TEQ performance may be warranted.

#### Modeling of Chemical Mixtures:

For [total](#) PCB modeling, Gobas has found that you should be able to get within a factor of 2 to 2.5 – these factors shouldn't be any higher. EPA cautions against modeling total PCBs and recommends focusing on individual congeners only, [although we are aware that much of the data for the site is Aroclor data, not congener data](#). The calibrated food web model was used to make predictions for chemical groups, e.g., total DDTs, total PCBs, PCB TEQs (birds), PCB TEQ (mammals), Dioxin TEQ (birds), and Dioxin TEQ (mammals). Predictions for mixtures are predicated upon have the correct weighted average  $K_{ow}$  of the mixture. If the composition of the mixture is not the same across the harbor, predictions will be inaccurate. For example, the SWAC for the surface sediment averages the total from each surface sample and if the compositions vary widely among surface samples, selecting an appropriate  $K_{ow}$  will be difficult. [In particular, the model TEQ predictions generally have the worst performance of any of the modeled chemicals. One possible method for improving the overall performance of the model would be to develop chemical specific food web models \(i.e. a PCB model, a DDT model, etc.\) instead of a single FWM with all chemicals incorporated into the single model.](#)

[Modeling chemicals individually, and then combining them after making the predictions avoids the messy averaging done prior to the making the food web predictions. This approach also permits some of the FWM species specific parameters to be adjusted for each chemical. In essence, one would have fish species calibrated for PCB uptake in the PCB model, DDT uptake in the DDT model, etc., instead of a “generic fish” calibrated to accumulate a number of chemicals. The SPAFs for the “generic” bass, sculpin etc. demonstrate that the model performs reasonably well \(i.e. SPAF < 5.0\) for most samples and chemicals, but could perform better if the species specific information were fine tuned for individual chemicals. This would also eliminate the problems with differing compositions of the mixture across the site. The predictiveness of the model might improve using this approach for mixtures. The time it would take to implement this approach must be weighed against whether the accuracy in the current version of the FWM is acceptable for its intended uses at Portland Harbor.](#)

#### Chemical Bioavailability:

A review of the data suggests that chemical bioavailability changes with increasing concentration of the chemical in the sediment on an organic carbon basis. For example, BSAFs decline with increasing concentration in the sediment. Because the laboratory testing confirms the field observation, it appears that the observed trend is real. There are a number reasons why chemical bioavailability could be changing. First, the presence of black carbon, and second, the presence

of oil/grease like phase. Both of these phases have much higher sorptive capacity for the organic contaminants of interest, and their presence in a harbor would not be unexpected.

Because the spreadsheets of data don't contain the organic carbon content of the sediments, it is not possible to determine if the BSAFs decrease with increasing organic carbon content. If so, this observation would point one in the direction of having a black carbon and/or oil/grease phases present.

The observation of declining bioavailability with increasing concentrations in the sediment clearly has implications for the development of sediment PRGs and the accuracy of long term tissue predictions through the hybrid model.

#### Quality of Field Data:

The development of BSAFs and the Portland Harbor food web are dependent upon the quality of the field data. Overall, EPA believes that the Portland Harbor RI/FS has generated high quality data, [although the amount of fish tissue is limited for some species. This limitation has contributed to a concern currently held by some reviewers is that the current iteration of the FWM may be overspecified \(i.e. too many parameters are included, or the data set is too small or too variable\).](#) However, a review of the some of the data during the review of the food web model has identified some anomalies. For example, the PCDD and PCDF data seem out of line with the PCBs in their bioaccumulation behavior. In addition, sediment sample "LWG0107R006SDS015C00" (located off-shore of Arkema) has usually high PCDF values relative to other samples and to its own PCDD levels; i.e., 2,3,7,8-TCDF is 14,000 pg/g while 2,3,7,8-TCDD is 5.4 pg/g, and other samples are 1,000-10,000 fold lower for 2,3,7,8-TCDF. EPA recommends a review of these results to ensure that the data is accurate.

#### Uncertainty and Variation in Sediment Concentrations:

[The uncertainty bounds of the tissue contaminant concentrations are of little use to site managers. These bounds represent the best and worst ability of the FWM to estimate a single data pair \(e.g. tissue PCBs and sediment PCBs\), not the range of uncertainty in the sediment concentrations in the environment that result in the specified fish concentrations. There is extensive discussion in Appendix E of the uncertainty and variation in the FWM predictions of chemical concentrations in tissues, but little discussion of uncertainty and variation in sediment concentrations that result in given tissue concentrations in fish or invertebrate species. The latter, uncertainty in sediment concentrations, the medium likely subject to remediation in Portland Harbor, is the information of value for site managers when making remedial decisions. The presented uncertainty results from the \(often estimated\) distributions around the model's parameters, many of which are estimated, non-site specific literature values. The bounds do not represent the uncertainty associated with measured concentrations or a model that was calibrated with empirical data. As such, it is impossible to know whether the uncertainty range is realistic, nor is its level of accuracy known with any certainty.](#)

[To prevent confusion in the future when discussion sediment contaminant concentrations that result in given tissue concentrations, it should be made clear when presenting the results that the](#)

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depicted confidence bounds do not represent the actual uncertainty of the sediment estimate. Instead, they only represent the variability in the food web model.

#### Next Steps and Recommendations:

EPA recommends validating the food web model using the Round 3 tissue data. Our cursory review of the new data shows that they are consistent with the data to calibrate the FWM and could provide a good validation set for the model. Assuming the model can be validated with the Round 3 data, all of the tissue data obtained during the RI should be combined and the model recalibrated to see if its predictive ability can be approved, particularly for PCB TEQs.

Food web models generally require a large number of input parameters. For the Arnot and Gobas model, 70 input parameters are required. As noted above, for the Portland Harbor site, 21 internal parameters were optimized resulting a total of 91 parameters being optimized. Given the limited number of average values used in the Monte Carlo process, the model appears to be highly calibrated to the field data used in the calibration process and what ever deficiencies exist in these data are captured in the calibration process. EPA recommends evaluating the model against the recently collected Round 3B tissue data to develop an understanding the accuracy of the predictions from Portland Harbor model. It is unclear whether the addition of the additional 21 parameters improves or reduces model performance. If the model does not perform well with the new data, EPA recommends reverting back to the uncalibrated Arnot and Gobas model.

In general, EPA recommends modeling each chemical individually, and then, combining them after making the predictions. This avoids the messy averaging done prior to the make the food web predictions and would also eliminate the problems with differing compositions of the mixture across the site. The predictive ability of the model might improve using this approach for mixtures.

#### **Specific Comments:**

##### Section 2.0 – Biota-Sediment Relationship Development:

Based on information presented in Appendix E and errata information presented on the Portland Harbor Portal, it is unclear whether a regression approach or an averaging approach was employed for the development of biota-sediment accumulation functions (BSAFs). Further, the report does not present the estimated BSAFs for benthic organisms (e.g., field and laboratory clams, crayfish, sculpin and laboratory worms). The approach for developing BSAFs and the estimated BSAFs should be clearly presented in the draft Remedial Investigation (RI) Report.

In general, EPA recommends the use of the paired approach rather than the regression approach. A quick review of the estimated BSAFs for clam tissue indicates a wide range in sample specific BSAFs. For example, calculated BSAFs for Aldrin in field clams range from 0.325 and 15. EPA believes that BSAFs should be evaluated to identify trends in the underlying ecological conditions at the sampling location (e.g., food web structure, sediment/water column

**Commented [MM2]:** I would like to be clear about next steps. On one hand, both Larry and Jennifer have recommended not calibrating the model. On the other hand, Larry seems to suggest a validation step using the Round 3B data. I have split the difference somewhat with my recommendation. Does this make sense?

relationships, chemical bioavailability, and diets/trophic levels of the organisms. BSAFs should be plotted spatially and plots of BSAF against lipid normalized tissue concentrations should be presented in addition to the plots of BSAF against organic carbon normalized sediment concentrations.

The plots of BSAF against concentrations of the chemical in the sediment on an organic carbon basis reveals a trend of decreasing BSAF with increase concentration in the sediment. For the laboratory derived BSAFs for worms and clams, the BSAFs are generally below 10 for low concentrations in sediment. Field clams BSAF have the same behavior. This generally argues against the use of a regression analysis to develop BSAFs and has implications for the performance of the food web model.

Although the regression analyses appear to have been properly performed, the equations in BSAF\_eqns\_shellfish\_052907.xls don't line up exactly with data in FieldClams\_BSAFs.xls. More significantly, some of the regressions have a low predictive power, (e.g., Aldrin has a  $r^2$  of 16% for shellfish). This further suggests that an averaging approach should be utilized.

EPA's independent review of the BSAFs across the site suggest that BSAFs may vary spatially across the site. Further evaluation of BSAF trends may prove useful in developing location specific BSAFs or developing additional normalization techniques that may reduce the uncertainty in BSAF estimates.

[In general, the BSAFs that can be calculated from predicted tissue concentrations and the empirical sediment data appear to be reasonable, and within the range of measured BSAFs at both Portland Harbor and at other sites. This is a good check on the operation and predictive ability of the FWM.](#)

#### Section 2.1 – Benthic Invertebrate/Sculpin BSAFs

BSAFs were developed for clams, crayfish and sculpin based on field collected data. In addition, BSAFs were developed for clams and worms based on laboratory bioaccumulation tests. Data was evaluated to determine whether an average paired BSAF or a regression line BSAF should be developed. Based on information presented in the report and the errata section of the Portland Harbor Portal, it appears that a regression approach was used to develop BSAFs for clam tissue and that this relationship was applied to all shellfish. However, it does not appear that the supporting information was included (e.g., strength of regression, statistical testing results, etc). Furthermore, no table is included in Appendix E that summarizes the BSAFs for field collected clams, crayfish and sculpin and laboratory testing of clams and worms. This information should be presented.

#### Section 2.2 – Demersal/Pelagic Fish BSAFs:

EPA does not believe it is appropriate to develop BSAFs for the majority of fish species collected at the Portland Harbor site. This recommendation is primarily based on the fact that the majority of fish species tested have limited contact with contaminated sediment, the

confounding factors of dietary and water column exposure, and uncertainty about where the fish may have come into contact with contaminated sediment. As a result, the only fish species (in addition to sculpin) for which BSAFs may reasonably be estimated are carp due to their propensity to accumulate chemicals, high lipid content and frequent contact with sediment during feeding.

### Section 3.2, Model Development and Methodology:

This section of the report identifies two key underlying assumptions of the Arnot and Gobas food web model: 1) The system is in steady state and 2) the flux between different media are governed by fugacity relationships. As a result of these assumptions, the food web model is expected to work best for chemicals that are subject to relatively fast exchange kinetic (e.g. lower  $K_{ow}$  substances) and small organisms because steady state will be achieved rapidly in these situations. The corollary is that the model should be used with caution in situation where the exchange kinetics are very slow (e.g. chemicals that are metabolized slowly or chemicals with high  $K_{ow}$  in large lipid rich organisms) because steady state takes a long time to achieve.

#### Section 3.2.5.1, Selection of Model Parameter Values and Distributions Used for Calibration:

EPA and the LWG agreed to consider a range of certain model parameters (dietary matrix, average water temperature, average body weights, average lipid content,  $K_{ow}$  and average sediment and water concentrations) in order to support a sensitivity analysis. However, the food web model varies many other parameters beyond this list such as moisture content, dietary absorption efficiency of lipid, dietary absorption efficiency of NLOM, dietary efficiency of water, and fraction of porewater ventilated. In addition to the input parameters a whole series of parameters, internal to the Arnot and Gobas model, were adjusted by using the Monte Carlo analysis. These additional internal parameters are: 1) Dietary absorption efficiencies for lipid (eL) and NLOM (eN); 2) phytoplankton uptake constants A and B; and 3) NLOM proportionality constant BETA. Dietary absorption efficiencies were optimized on a species specific basis. These parameters are presented in Tables 3-5 to 3-9.

Examination of Tables 3-5, 3-6, and 3-7 reveals that the calibrated values for environmental, general biological, and species-specific parameters are largely unchanged from those used by Arnot & Gobas except for: 1) Crayfish dietary absorption efficiency of lipid and NLOM; 2) clams dietary absorption efficiency of lipid; and 3) phytoplankton uptake constants A and B.

From Tables 3-5, 3-6, 3-7 and 3-8, there are: Four environmental parameters, three general biological parameters of which three are internal parameters; fifty-two species-specific biological parameters of which eighteen are internal parameters; and thirty-two species-specific dietary parameters. This results in ninety-one total parameters (of which 21 are Arnot & Gobas internal parameters) that are optimized in the Monte Carlo procedure. There are 10 different species in the food web and only 5 of the species (clams, carp, crayfish, sculpin, and smallmouth bass) have values for PCBs 17, 170 and 206. These five values are used in calibrating the model, i.e., providing the "calibrated" values reported in Tables 3-5, 3-6, 3-7 and 3-8. It is unclear how the "calibrated" values for the largescale sucker and northern pikeminnow are derived using PCBs 17, 170, and 206 when these species have no data for these congeners (see Appendix E2, Table

**Commented [MM3]:** I added this comment based on a statement Burt has made in the past. However, we will be developing tissue-residue TRVs for more chemicals than are modeled in the FWM and for more fish species than carp. How do we develop PRGs for these chemicals and fish if we do not apply a BSAF. Maybe it is better to develop BSAFs for species other than carp and just acknowledge the uncertainty.



1). For the lower trophic levels, i.e., phytoplankton, zooplankton, and benthic invertebrates, their calibrated values can be found based upon the their predator residues.

[EPA has previously expressed concern regarding the selection of PCB congeners 17, 170 and 206 to calibrate the model. The logic for the selection provided by LWG, based in part on the spread of the log  \$K\_{ow}\$  values for the three congeners, could be met by calibrating on several of the more abundant PCB congeners.](#)

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In general, Arnot and Gobas do not recommend calibrating the food web model as long as the model is used with its application domain. However, unless sufficient information (e.g., site specific empirical data) is available to represent these parameters as a robust distribution or unless we have conducted additional site specific studies to justify a change to the value, EPA recommends against modifying the values to get better agreement between the model and tissue. This is especially true given the inherent uncertainties of the data set and the dynamic nature of the Willamette River.

In light of the additional parameterization of the model, it is important to check whether the model calculations are consistent with available empirical data such that confidence in the model is gained. This has the same objective of calibration, but it is more of a hypothesis testing scenario, where the model outcomes are compared with independent data (data not used in the construction of the model). In this case, the preferred model outcome is the chemical concentration in a particular species, and involves the comparison of observed and predicted concentrations in different aquatic species.

Table 3-7 presents “calibrated values” for weight, lipid content, etc. for each species. However, instead of taking this approach, a rigorous evaluation of how well the model outcomes match tissue observations in Portland Harbor should be performed. In order to evaluate how well the model outcomes match the observations, Gobas uses the mean model bias MB to express the central tendency of the model. MB is the geometric mean (assuming a log-normal distribution) of the ratio of predicted and observed concentrations. Equation 3 on page 13 presents a similar equation. However, this equation does not appear to use a log-normal distribution, and does not appear to use information from a number of observations from each species (it looks like one average is used).

From a modeling perspective, the model codes are those of Arnot and Gobas and the only differences between the Portland Harbor model and the Arnot & Gobas model are the values for the 21 internal parameters discussed above. EPA would like to point out that Arnot and Gobas went to great lengths in assembling data that were of high quality across a number of food webs and these data have coverage of all species in these food webs. Subsequently, they used these data to validate their model. The effort here assumes that the Portland Harbor data are of higher quality or otherwise better than that used by Arnot and Gobas. However, given the complex nature of the Portland Harbor site and issues related to bioavailability, it is unclear whether the Portland Harbor data are of higher quality. In addition, it is unclear how the 21 internal parameters were selected for optimization; why not all the parameters in the model such as equations for growth and -respiration? The modeling approach presented in Appendix E suggests that by optimizing these 21 internal parameters, the Portland Harbor model will have

better predictive power than the Arnot & Gobas model. Mathematically with the 5 average values, the Portland Harbor model does provide a good fit, i.e., SPAFs are small. However it is likely that the Arnot and Gobas model (with Arnot and Gobas parameterization) would provide similar fits.

Although EPA questions the appropriateness of the calibration step, it does not appear that the execution of the Monte Carlo technique was performed improperly. The SPAFs, and sensitivity and uncertainty analyses demonstrates that Portland Harbor model does fit the field data from the site reasonably well. These analyses don't speak or address the issue of the quality of field data.

The tissue data set used to develop the FWM, particularly for most fish species, is very limited. The available Round 3 tissue data should be used to validate the existing model. If the FWM can be validated, all of the tissue data from the RI should be pooled to develop the final calibrated model. This step should help lessen the overspecification issues with the FWM. The quality of the predictions from the Portland Harbor model are predicated upon the quality of the field data and if quality of the data is low, the model will provide poor predictions, in essence, garbage in – garbage out. To address the issue of the quality of the field data, additional data sets from time periods totally independent of the calibration data are required. With these data, predictions based upon the conditions (concentrations of chemical in sediment and water) can be made and then, compared to independent data. These would provide a much better indication of the predictive power of the Portland Harbor model.

Given the number of parameters being optimized with the Monte Carlo technique and the relatively limited amounts of the field data, the model seems over parameterized. Without the 21 internal parameters, there are 70 input values being optimized with the Monte Carlo technique. Of the 70 inputs values, 32 are diet, 9 are weight, 10 are lipid content, and 10 are moisture content, and all of these values are required input values for the model. Unfortunately, this is the nature of food web **model**.

**Commented [MM4]:** There are a lot of comments from Jennifer and Larry regarding the parameterization step. These need to be reviewed for flow and consistency. I took my best shot.

#### Section 3.2.5.1.1 – Chemical Concentrations in Water:

Understanding the relative contribution of sediment contaminants and water contaminants to fish tissue levels is critical from the standpoint of PRG development. The appropriate place to perform this analysis is with the empirical data prior to PRG development. There are multiple possibilities in achieving acceptable fish tissue concentrations with the back calculation. The most straight forward way to address this question is with the use of empirical data. This will entail a discussion on how water is handled in the model. EPA believes that use of a total water concentration **s** overestimates the tendency of contaminant in water to partition to fish tissue. This is especially true where a lot of TSS or particulate organic matter is present in the water. The chemical will be bound up on particulates and not very available to the fish. As a result, dissolved measurements from the field should be utilized to ensure that this overestimate does not occur. In this version of the food web model, a generic equation was applied to go from total to dissolved concentrations. EPA believes that the use of empirical surface water data is preferable to a calculated estimate in order to avoid over or under estimating the contribution from the water column.

#### Section 3.2.5.5 - Uncertainty Assessment:

The role of any uncertainty analysis should be to assess the error in the model calculations, which is important because the magnitude of the model needs to be considered when interpreting the results of the model calculations for management purposes. The comparisons of predicted and observed results in an uncertainty analysis can be plotted as a distribution of predicted and observed ratios. A rigorous analysis of observed versus predicted data variability may be used to develop estimates of model uncertainty. In an uncertainty analysis, many parameters are correlated, so it is difficult to apply Monte Carlo simulations of uncertainty. One of the key requirements is that the model state variables are independent. Examples of related state variables are animal size, growth rate, lipid content and feeding rate. In addition, a true uncertainty analysis will evaluate uncertainty in each model parameter.

For uncertainty analysis, the parameters you can include and still maintain independence include lipid content, temperature and  $K_{ow}$ . ~~He does~~[We do](#) not recommend conducting an uncertainty analysis on prey composition, but can use a sensitivity analysis to see how much of a difference prey assumptions would make (see above comment).

#### Section 3.5.2 – Application of the Model at Smaller Spatial Scales:

The harbor wide calibrated Portland Harbor food web model was executed at smaller scales and on laboratory test data. In general, the fits (SPAFs) were poorer, and these results were not surprising given that the model is highly calibrated to harbor wide average values.

#### **Summary Comments**

The Arnot and Gobas model has been used with modification to 21 internal parameters. The Portland Harbor model is high calibrated with field data from the site. The calculations with the model appear to have been done correctly. The regression equations for predicting residues in tissue based upon concentration of chemical in the sediment were done correctly. There tends to be a lot scatter in the data, and I wonder if the regressions have any predictive ability. Many of the predictions were done for mixtures, and if the composition of the mixture changes across the harbor, then predictions will be inaccurate and have high uncertainty. (This issue is not addressed in Appendix E.) This influences both food web predictions and BSAF calculations. The inverse dependence of BSAFs upon concentration of the chemical in sediment on an organic carbon basis indicates that bioavailability changes with increasing concentration in the sediment. This issue isn't addressed in the SWAC calculation while the field measured BSAFs incorporate these influences.